LH
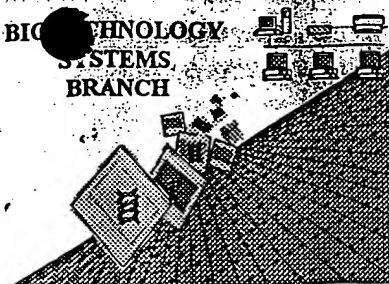
# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:  _09/820,843_

Source:  _OIPE_

Date Processed by STIC:  _4/18/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER,  703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX,  703-308-4216.
PATENTIN 2.1 e-mail help:  patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help:  patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE.  SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

# Raw Sequence Listing Error Summary

**ERROR DETECTED**    **SUGGESTED CORRECTION**      SERIAL NUMBER: _09/820,843_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 \_\_\_\_   Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 \_\_\_\_   Wrapped Aminos    The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 \_\_\_\_   Incorrect Line Length    The rules require that a line not exceed 72 characters in length. This includes spaces.

4 \_\_\_\_   Misaligned Amino Acid Numbering    The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 \_\_\_\_   Non-ASCII    This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 \_\_\_\_   Variable Length    Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing

7 \_\_\_\_   PatentIn ver. 2.0 "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 \_\_\_\_   Skipped Sequences (OLD RULES)    Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 \_\_\_\_   Skipped Sequences (NEW RULES)    Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 \_\_\_\_   Use of n's or Xaa's (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 \_\_\_\_   Use of "Artificial" (NEW RULES)    Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 \_\_\_\_   Use of <220>Feature (NEW RULES)    Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
**(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)**    (Sec. 1.823 of new Rules)

13 \_\_\_\_   PatentIn ver. 2.0 "bug"    **Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.**

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/820,843

DATE: 04/18/2001
TIME: 07:35:07  Does Not Comply
Corrected Diskette Needed

*see p. 6, too*

Input Set : A:\ES.txt
Output Set: N:\CRF3\04182001\I820843.raw

14 <210> SEQ ID NO: 1
15 <211> LENGTH: 51
16 <212> TYPE: PRT
17 <213> ORGANISM: C. jejuni
19 <220> FEATURE:

*use underscore, not hyphen*

20 <221> NAME/KEY: misc-feature    misc_feature
21 <223> OTHER INFORMATION: highly acidic protein
24 <220> FEATURE:
25 <221> NAME/KEY: misc-feature
26 <223> OTHER INFORMATION: gi|6967728
29 <400> SEQUENCE: 1
31 Met Ala Tyr Glu Asp Glu Glu Asp Leu Asn Tyr Asp Asp Tyr Glu Asn
32 1               5                   10                  15
34 Glu Asp Glu Glu Tyr Pro Gln Asn His His Lys Asn Tyr Asn Tyr Asp
35              20                  25                  30
37 Asp Asp Asp Tyr Glu Tyr Asp Asp Asp Asn Asn Asp Asp Asp Phe Tyr
38           35                  40                  45
40 Glu Met Asp
41        50
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 32
45 <212> TYPE: PRT
46 <213> ORGANISM: C. jejuni
48 <220> FEATURE:
49 <221> NAME/KEY: misc_feature
50 <223> OTHER INFORMATION: small hydrophobic protein
53 <220> FEATURE:
54 <221> NAME/KEY: misc_feature
55 <223> OTHER INFORMATION: gi|6969129
58 <400> SEQUENCE: 2
60 Met Thr Met Leu Asp Ile Phe Glu Ile Ile Phe Ile Thr Thr Val Val
61 1               5                   10                  15
63 Ile Ile Gly Phe Gly Gly Ile Val Phe Val Val Thr Lys Glu Lys Lys
64              20                  25                  30
66 <210> SEQ ID NO: 3
67 <211> LENGTH: 57
68 <212> TYPE: PRT
69 <213> ORGANISM: C. jejuni
71 <220> FEATURE:

```
72 <221> NAME/KEY: misc_feature
73 <223> OTHER INFORMATION: putative coiled coil protein
76 <220> FEATURE:
77 <221> NAME/KEY: misc_feature
78 <223> OTHER INFORMATION: gi|6968493
81 <400> SEQUENCE: 3
83 Met Ser Phe Glu Glu Asn Leu Lys His Ala Asn Glu Ser Leu Glu Lys
84 1               5                   10                  15
86 Leu Asn Asn Gln Glu Leu Ala Leu Asp Glu Ser Val Lys Ile Tyr Lys
87              20                  25                  30
89 Glu Gly Leu Glu Ser Ile Lys Lys Ala Arg Leu Glu Leu Glu Lys Ala
90          35                  40                  45
92 Lys Leu Glu Val Glu Gln Ile Asp Glu
93       50                  55
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 542
97 <212> TYPE: PRT
98 <213> ORGANISM: C. jejuni
100 <220> FEATURE:
101 <221> NAME/KEY: misc_feature
102 <223> OTHER INFORMATION: highly acidic protein
105 <220> FEATURE:
106 <221> NAME/KEY: misc_feature
107 <223> OTHER INFORMATION: gi|6968611
110 <400> SEQUENCE: 4
112 Met Lys Ile Leu Leu Leu Asn Glu Asn Pro Val Val Ser Arg Leu Val
113 1               5                   10                  15
115 Ser Leu Ser Ala Lys Lys Met Ser Tyr Asp Phe Glu Glu Leu Asn Ala
116              20                  25                  30
118 Tyr Ser Glu Asn Leu Gly Asn Tyr Asp Val Ile Val Val Asp Ser Asp
119          35                  40                  45
121 Thr Pro Ala Pro Leu Lys Ile Leu Lys Glu Lys Cys Asp Arg Leu Ile
122      50                  55                  60
124 Phe Leu Ala Pro Arg Asn Gln Asn Val Glu Asp Ile Asp Ala Gln Ile
125 65                  70                  75                  80
127 Leu Gln Lys Pro Phe Leu Pro Thr Asp Phe Leu Asn Leu Leu Asn Asn
128              85                  90                  95
130 Lys Asp Ala Asn Lys His Thr Ser Ile Asp Leu Pro Met Leu Ser Asn
131             100                 105                 110
133 Asp Glu Asn Pro Tyr Ala Asp Ile Ser Leu Asp Leu Asp Asn Leu Asn
134             115                 120                 125
136 Leu Asp Asp Leu Pro Asp Glu Asn Ser Leu Asp Ile Asn Ser Glu Gly
137      130                 135                 140
139 Met Glu Asp Leu Ser Phe Asp Asp Asp Ala Gln Asp Asp Asn Ala Asn
140 145                 150                 155                 160
142 Lys Thr Leu Glu Thr Gln Asn Leu Glu His Glu Thr Ile Lys Glu Gln
143             165                 170                 175
145 Thr Gln Glu Asp Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly
146             180                 185                 190
```

RAW SEQUENCE LISTING  DATE: 04/18/2001
PATENT APPLICATION: US/09/820,843  TIME: 07:35:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\04182001\I820843.raw

```
148 Glu Ser Glu Lys Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr
149          195                200                205
151 Glu Pro Ser Leu Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu
152      210                215                220
154 Ile Lys Glu Asp Asp Lys Asn Glu Glu Ile Glu Lys Gln Glu Leu Leu
155 225                230                235                240
157 Asp Asp Ser Lys Thr Asn Thr Leu Glu Met Gln Glu Glu Leu Ser Glu
158          245                250                255
160 Ser Gln Asp Asp Asn Ser Asn Lys Thr Leu Glu Thr Gln Asn Leu Glu
161          260                265                270
163 His Asp Asn Leu Glu Gln Glu Thr Ile Lys Glu Gln Thr Gln Glu Asp
164          275                280                285
166 Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly Glu Ser Glu Lys
167      290                295                300
169 Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr Glu Pro Ser Leu
170 305                310                315                320
172 Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu Asp Asn Lys Glu
173          325                330                335
175 Leu Gln Ala Asn Ile Ser Asp Phe Asp Asp Leu Pro Glu Val Glu Glu
176          340                345                350
178 Gln Glu Lys Glu Met Asp Phe Asp Asp Leu Pro Glu Asp Ala Glu Phe
179          355                360                365
181 Leu Gly Gln Ala Lys Tyr Asn Glu Glu Ser Glu Glu Asn Leu Glu Glu
182      370                375                380
184 Phe Ala Pro Val Val Glu Glu Asp Ile Gln Asp Glu Ile Asp Asp Phe
185 385                390                395                400
187 Ala Ser Asn Leu Ser Thr Gln Asp Gln Ile Lys Glu Glu Leu Ala Gln
188          405                410                415
190 Leu Asp Glu Leu Asp Tyr Gly Ile Asp Ser Asp Asn Ser Ser Lys Val
191          420                425                430
193 Leu Glu Asp Phe Lys Asp Glu Pro Ile Leu Asp Asp Lys Glu Leu Gly
194          435                440                445
196 Thr Asn Glu Glu Glu Val Val Val Pro Asn Leu Asn Ile Ser Asp Phe
197      450                455                460
199 Asp Thr Leu Lys Glu Ser Asp Ile Gln Glu Ala Leu Gly Glu Glu Ile
200 465                470                475                480
202 Leu Glu Lys Asn Glu Glu Pro Ile Val Ser Asp Val Thr Lys Asp Asp
203          485                490                495
205 Asn Ser Glu Glu Ile Val Asn Glu Leu Ser Gln Ser Ile Ala Gly Ala
206          500                505                510
208 Ile Thr Ser Ser Ile Lys Asp Asp Thr Leu Lys Ala Ala Leu Lys Gly
209          515                520                525
211 Met Asn Met Asn Ile Asn Ile Asn Ile Ser Phe Lys Glu Asp
212      530                535                540
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 172
216 <212> TYPE: PRT
217 <213> ORGANISM: C. pneumoniaeCWL029
219 <220> FEATURE:
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RAW SEQUENCE LISTING                    DATE: 04/18/2001
PATENT APPLICATION:   US/09/820,843     TIME: 07:35:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\04182001\I820843.raw

220 <221> NAME/KEY: misc_feature
221 <223> OTHER INFORMATION: histone like protein 2
224 <220> FEATURE:
225 <221> NAME/KEY: misc_feature
226 <223> OTHER INFORMATION: gi|4376663
229 <400> SEQUENCE: 5
231 Met Ile Gly Ala Gln Lys Lys Gln Ser Gly Lys Lys Thr Ala Ser Arg
232 1               5                   10                  15
234 Ala Val Arg Lys Pro Ala Lys Lys Val Ala Ala Lys Arg Thr Val Lys
235             20                  25                  30
237 Lys Ala Thr Val Arg Lys Thr Ala Val Lys Lys Pro Ala Val Arg Lys
238         35                  40                  45
240 Thr Ala Ala Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg Thr
241     50                  55                  60
243 Val Arg Lys Thr Val Ala Lys Lys Pro Ala Val Lys Lys Val Ala Ala
244 65                  70                  75                  80
246 Lys Arg Val Val Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg
247             85                  90                  95
249 Ala Val Arg Lys Thr Val Ala Lys Lys Pro Val Ala Arg Lys Thr Thr
250             100                 105                 110
252 Val Ala Lys Gly Ser Pro Lys Lys Ala Ala Ala Cys Ala Leu Ala Cys
253         115                 120                 125
255 His Lys Asn His Lys His Thr Ser Ser Cys Lys Arg Val Cys Ser Ser
256         130                 135                 140
258 Thr Ala Thr Arg Lys His Gly Ser Lys Ser Arg Val Arg Thr Ala His
259 145                 150                 155                 160
261 Gly Trp Arg His Gln Leu Ile Lys Met Met Ser Arg
262                 165                 170
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 63
266 <212> TYPE: PRT
267 <213> ORGANISM: C. trachomatis
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <223> OTHER INFORMATION: hypothetical protein-possible frameshift with CT593
274 <220> FEATURE:
275 <221> NAME/KEY: misc_feature
276 <223> OTHER INFORMATION: gi|3522902
279 <400> SEQUENCE: 6
281 Met Phe Thr Leu Phe Leu Cys Glu His Leu Leu Thr Asn Ile Leu Ala
282 1               5                   10                  15
284 Ser Ser Phe Leu Ala Lys Ser Gln Gly Phe Ile Thr Leu Val Asn Leu
285             20                  25                  30
287 Phe His Lys Ile Pro Gly Leu Lys Val Ile Glu Ile Thr Cys Leu Ala
288         35                  40                  45
290 Leu Pro Leu Gly Ile His Ser Ile Ile Gly Phe Ser Tyr Leu Leu
291     50                  55                  60
293 <210> SEQ ID NO: 7
294 <211> LENGTH: 203

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295 <212> TYPE: PRT
296 <213> ORGANISM: C. trachomatis
298 <220> FEATURE:
299 <221> NAME/KEY: misc_feature
300 <223> OTHER INFORMATION: histone like protein 2
303 <220> FEATURE:
304 <221> NAME/KEY: misc_feature
305 <223> OTHER INFORMATION: gi|3328438
308 <400> SEQUENCE: 7
310 Met Asn Met Leu Gly Val Gln Lys Lys Cys Ser Thr Arg Lys Thr Ala
311 1               5                   10                  15
313 Ala Arg Lys Thr Val Val Arg Lys Pro Ala Ala Lys Lys Thr Ala Ala
314             20                  25                  30
316 Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys Thr Val Ala Arg
317         35                  40                  45
319 Lys Thr Val Ala Lys Lys Thr Val Ala Ala Arg Lys Pro Val Ala Lys
320     50                  55                  60
322 Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys
323 65                  70                  75                  80
325 Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val Ala Ala Arg Lys
326             85                  90                  95
328 Pro Val Ala Lys Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Ala
329             100                 105                 110
331 Val Ala Lys Lys Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val
332             115                 120                 125
334 Ala Ala Arg Lys Pro Val Ala Lys Arg Val Ala Ser Thr Lys Lys Ser
335     130                 135                 140
337 Ser Ile Ala Val Lys Ala Gly Val Cys Met Lys Lys His Lys His Thr
338 145                 150                 155                 160
340 Ala Ala Cys Gly Arg Val Ala Ala Ser Gly Val Lys Val Cys Ala Ser
341             165                 170                 175
343 Ala Ala Lys Arg Lys Thr Asn Pro Asn Arg Ser Arg Thr Ala His Ser
344             180                 185                 190
346 Trp Arg Gln Gln Leu Met Lys Leu Val Ala Arg
347         195                 200
349 <210> SEQ ID NO: 8
350 <211> LENGTH: 372
351 <212> TYPE: PRT
352 <213> ORGANISM: H. influenzae
354 <220> FEATURE:
355 <221> NAME/KEY: misc_feature
356 <223> OTHER INFORMATION: outer membrane integrity protein (tolA)
359 <220> FEATURE:
360 <221> NAME/KEY: misc_feature
361 <223> OTHER INFORMATION: gi|1573353
364 <400> SEQUENCE: 8
366 Met Gln Asn Asn Arg Gln Lys Lys Gly Ile Asn Ala Phe Ala Ile Ser
367 1               5                   10                  15
369 Ile Leu Leu His Phe Ile Leu Phe Gly Leu Leu Ile Leu Ser Ser Leu
```

```
<210>   32
<211>   497
<212>   PRT
<213>   B. burgdorferi

<220>
<221>   misc_feature
<223>   predicted coding region BB0553


<220>
<221>   misc_feature
<223>   gi|2688482


<400>   32

Met Asn Lys Thr Lys Asn Arg Ser Leu Thr Tyr Phe Ile Ile Leu Ser
1               5                  10                  15

Cys Ile Ser Leu Phe Gly Ala Asn Asn Asn Thr Ile Ser Tyr Ser Ser
            20                  25                  30

Ile Glu Ile Pro Leu Glu Asp Leu Ser Glu Glu Phe Lys Ser Ser Gly
        35                  40                  45

Asn Lys Ser Asp Gln Ile Asn Thr Ser Lys His Leu Asn Lys Asn Ile
    50                  55                  60

Val Ser Tyr Glu Asp Pro Lys Lys Gly Lys Asp Leu Lys Leu Pro Glu
65                  70                  75                  80

Asn Ile Arg Asp Lys Lys Leu Pro Gln Lys Arg Met Asp Glu Asn Asp
                85                  90                  95

Leu Lys Ser Val Ile Glu Asn Tyr Glu Asn Lys Ile Lys Asn Ile Glu
            100                 105                 110

Lys Leu Leu Lys Thr Lys Asn Gln Lys Thr Ser Glu Asn Glu Asn Lys
            115                 120                 125

Lys Ile Glu Ser Ile Glu Lys Lys Ala Lys Lys Tyr Glu Ile Leu Thr
    130                 135                 140

Asn Lys Leu Lys Asn Glu Ile Val Glu Ile Lys Lys Leu Leu Asn Lys
145                 150                 155                 160

Lys Ile Lys Pro Lys Glu Asp Glu Asn Tyr Glu Lys Ile Asn Ile Glu
                165                 170                 175

Asn Ile Glu Glu Glu Thr Asp Asp Asp Phe Glu Asp Asn Tyr Glu Tyr
            180                 185                 190

Asn Asp Glu Ile Glu Xaa Thr Asn Glu Asp Asn Tyr Pro Ser Asn Glu
    195                 200                 205

Gly Ile Ile Asn Asn Leu Lys Glu Asn Leu Asn Glu Asn Glu Lys Tyr
```

only the
erased
portion of
Sequence 32
shown

→ see item 10
on Error
Summary
Sheet

Input Set : A:\ES.txt
Output Set: N:\CRF3\04182001\I820843.raw

```
L:10   M:270 C: Current Application Number differs, Replaced Current Application No
L:10   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20   M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:25   M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:2886 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:2886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:4688 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
L:4688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
```

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re application of

Samir Kumar BRAHMACHARI et al.

Appln. No.: 09/820,843                   Group Art Unit: Not Yet Assigned

Filed: March 30, 2001                    Examiner: Not Yet Assigned

Confirmation number: 7045

For:   A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE
       PROTEINS USEFUL AS ANTI-INFECTIVES

<div align="center">

**STATEMENT TO SUPPORT FILING AND SUBMISSION IN**

**ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825**

</div>

Assistant Commissioner for Patents
Washington, D.C.  20231
**Box SEQUENCE**

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned

hereby states that:

1.      the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not

include any new matter;

2.      the content of the attached paper copy and the attached computer readable copy of

the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively,

are the same; and

3.      all statements made herein of my own knowledge are true and that all statements

made on information and belief are believed to be true, and further, that these statements were

made with the knowledge that willful false statements and the like so made are punishable by

fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that

such willful false statements may jeopardize the validity of the application or any patent resulting

therefrom.

Respectfully submitted,

Drew Hissong
Registration No. 44,765

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   MACPEAK & SEAS, PLLC
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Telephone:  (202) 293-7060
Facsimile:  (202) 293-7860

Date:  May 18, 2001